```
=> d his

        (FILE 'HOME' ENTERED AT 08:02:59 ON 07 JUN 2006)

        FILE 'CAPLUS, BIOSIS, MEDLINE' ENTERED AT 08:03:12 ON 07 JUN 2006
L1          8717 S GLP
L2         82674 S GLUCAGON
L3          5555 S L1 (L) L2
L4          4131 S PIOGLITAZONE
L5          5040 S ROSIGLITAZONE
L6             1 S THIOGLITAZONE
L7          1355 S TZD
L8             6 S L3 (L) L4
L9           858 S L4 (L) L5
L10            0 S L9 AND L3
L11           40 S L1 AND L4
L12           36 S L1 AND L5
L13           33 S L11 (L) L12
L14           33 DUP REM L13 (0 DUPLICATES REMOVED)
L15            3 S L14 AND PY<2002
               E YAKUBU MADUS /AU
L16           11 S E4 OR E5 OR E6
               E EDWARD STRAMM /AU
               E EDWARDS STRAMM /AU
               E JOHNSON WILLIAM /AU
L17          164 S E3 OR E4
               E LOIUS VIGNATI /AU
               E LOUIS VIGNATI /AU
L18            1 S E3
L19            0 S L16 (L) L17
L20            0 S L16 (L) L18
L21            1 S L16 AND GLP
```

SCORE Search Results Details for Application 10679746 and Search Result us-10-679-746-1.p2n.rge.

This page gives you Search Results detail for the Application 10679746 and Search Result us-10-679-746-1.p2n.rge.

start

```
                        GenCore version 5.1.8
               Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:         May  7, 2006, 02:01:05 ; Search time 3043 Seconds
                                        (without alignments)
                                        840.603 Million cell updates/sec

Title:          US-10-679-746-1
Perfect score:  155
Sequence:       1 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 30

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:      11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679746/runat_05052006_121837_15755/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10679746_@CGN_1_1_4939_@runat_05052006_121837_15755 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      GenEmbl:*
                1:  gb_ba:*
```

```
 2:  gb_in:*
 3:  gb_env:*
 4:  gb_om:*
 5:  gb_ov:*
 6:  gb_pat:*
 7:  gb_ph:*
 8:  gb_pr:*
 9:  gb_ro:*
10:  gb_sts:*
11:  gb_sy:*
12:  gb_un:*
13:  gb_vi:*
14:  gb_htg:*
15:  gb_pl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	155	100.0	111	6	CS077318	CS077318 Sequence
2	155	100.0	144	6	AR030619	AR030619 Sequence
3	155	100.0	144	6	AR168157	AR168157 Sequence
4	155	100.0	228	6	AX840858	AX840858 Sequence
5	155	100.0	277	9	RATGLU4	K02811 Rat glucago
6	155	100.0	315	6	I07551	I07551 Sequence 40
7	155	100.0	396	6	AX147675	AX147675 Sequence
8	155	100.0	528	6	AR030614	AR030614 Sequence
9	155	100.0	528	6	AR030615	AR030615 Sequence
10	155	100.0	528	6	AR168152	AR168152 Sequence
11	155	100.0	528	6	AR168153	AR168153 Sequence
12	155	100.0	528	6	E05860	E05860 DNA encodin
13	155	100.0	543	6	CS077314	CS077314 Sequence
14	155	100.0	543	8	BT006813	BT006813 Homo sapi
15	155	100.0	543	11	AY890068	AY890068 Synthetic
16	155	100.0	543	11	AY890069	AY890069 Synthetic
17	155	100.0	543	11	AY892547	AY892547 Synthetic
18	155	100.0	543	11	AY892548	AY892548 Synthetic
19	155	100.0	543	11	BT007507	BT007507 Synthetic
20	155	100.0	559	4	AF529185	AF529185 Ovis arie
21	155	100.0	574	4	AY242124	AY242124 Sus scrof
22	155	100.0	668	9	MMPPROGLG	Z46845 M.musculus
23	155	100.0	707	4	AY588290	AY588290 Capra hir
24	155	100.0	895	6	AR108106	AR108106 Sequence
25	155	100.0	955	6	AR108107	AR108107 Sequence
26	155	100.0	955	6	AR108109	AR108109 Sequence
27	155	100.0	1034	6	A31421	A31421 H.sapiens m
28	155	100.0	1034	6	AR634243	AR634243 Sequence
29	155	100.0	1036	6	CQ729100	CQ729100 Sequence
30	155	100.0	1053	9	GPIGG	D00014 Cavia porce
31	155	100.0	1062	6	AR270649	AR270649 Sequence
32	155	100.0	1062	8	HUMGLUC	J04040 Human gluca
33	155	100.0	1102	9	BC012975	BC012975 Mus muscu
34	155	100.0	1104	9	OCOGLU	M57688 Octodon deg
35	155	100.0	1108	4	BOVGG	K00107 Bovine panc
36	155	100.0	1116	9	AF276754	AF276754 Mus muscu
37	155	100.0	1118	9	HAMGG	J00059 Syrian hams

SCORE Search Results Details for Application 10679746 and Search Result us-10-679-746-1.p2n.rnpbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10679746 and Search Result us-10-6: 1.p2n.rnpbm.

start

Go Back to prev

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 7, 2006, 02:28:45 ; Search time 536 Seconds
                                           (without alignments)
                                           694.257 Million cell updates/sec

Title: US-10-679-746-1
Perfect score: 155
Sequence: 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 30

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679746/runat_05052006_121846_15907/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10679746_@CGN_1_1_1026_@runat_05052006_121846_15907 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

```
 2:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 3:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
 4:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
 5:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 6:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 7:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 8:  /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
 9:  /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10:  /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	155	100.0	90	6	US-10-378-094-49	Sequence 49, Appl
2	155	100.0	90	9	US-10-997-078-51	Sequence 51, Appl
3	155	100.0	90	9	US-10-997-700-24	Sequence 24, Appl
4	155	100.0	93	9	US-10-997-078-52	Sequence 52, Appl
5	155	100.0	93	9	US-10-997-700-25	Sequence 25, Appl
6	155	100.0	112	5	US-10-093-958-18	Sequence 18, Appl
7	155	100.0	180	6	US-10-378-094-50	Sequence 50, Appl
c 8	155	100.0	180	6	US-10-378-094-51	Sequence 51, Appl
9	155	100.0	180	9	US-10-775-180-417	Sequence 417, App
10	155	100.0	180	9	US-10-775-180-418	Sequence 418, App
11	155	100.0	180	9	US-10-775-204-1221	Sequence 1221, Ap
12	155	100.0	180	9	US-10-775-204-1222	Sequence 1222, Ap
13	155	100.0	228	6	US-10-097-230-6	Sequence 6, Appli
14	155	100.0	231	9	US-10-775-180-537	Sequence 537, App
15	155	100.0	231	9	US-10-775-204-1458	Sequence 1458, Ap
16	155	100.0	249	9	US-10-775-180-536	Sequence 536, App
17	155	100.0	249	9	US-10-775-204-1457	Sequence 1457, Ap
18	155	100.0	261	9	US-10-997-700-83	Sequence 83, Appl
19	155	100.0	265	9	US-10-997-700-81	Sequence 81, Appl
20	155	100.0	267	9	US-10-997-700-85	Sequence 85, Appl
21	155	100.0	273	9	US-10-997-078-145	Sequence 145, App
22	155	100.0	435	9	US-10-775-180-535	Sequence 535, App
23	155	100.0	435	9	US-10-775-204-1456	Sequence 1456, Ap
24	155	100.0	517	5	US-10-060-036-3938	Sequence 3938, Ap
25	155	100.0	543	9	US-10-775-180-60	Sequence 60, Appl
26	155	100.0	543	9	US-10-775-180-61	Sequence 61, Appl
27	155	100.0	543	9	US-10-775-180-62	Sequence 62, Appl
28	155	100.0	543	9	US-10-775-180-63	Sequence 63, Appl
29	155	100.0	543	9	US-10-775-180-412	Sequence 412, App
30	155	100.0	543	9	US-10-775-180-413	Sequence 413, App
31	155	100.0	543	9	US-10-775-180-414	Sequence 414, App
32	155	100.0	543	9	US-10-775-180-415	Sequence 415, App
33	155	100.0	543	9	US-10-775-180-416	Sequence 416, App
34	155	100.0	543	9	US-10-775-180-499	Sequence 499, App
35	155	100.0	543	9	US-10-775-180-523	Sequence 523, App
36	155	100.0	543	9	US-10-775-180-524	Sequence 524, App
37	155	100.0	543	9	US-10-775-204-198	Sequence 198, App
38	155	100.0	543	9	US-10-775-204-200	Sequence 200, App
39	155	100.0	543	9	US-10-775-204-201	Sequence 201, App
40	155	100.0	543	9	US-10-775-204-202	Sequence 202, App
41	155	100.0	543	9	US-10-775-204-1216	Sequence 1216, Ap
42	155	100.0	543	9	US-10-775-204-1217	Sequence 1217, Ap

SCORE Search Results Details for Application 10679746 and Search Result us-10-679-746-1.p2n.rnpbn.

This page gives you Search Results detail for the Application 10679746 and Search Result us-10-679-746-1.p2n.rnpbn.

start

```
                       GenCore version 5.1.8
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:           May  7, 2006, 02:33:50 ; Search time 450 Seconds
                                         (without alignments)
                                         407.254 Million cell updates/sec

Title:            US-10-679-746-1
Perfect score:    155
Sequence:         1 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 30

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0

Searched:         9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters:        18612856

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679746/runat_05052006_121849_15963/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10679746_@CGN_1_1_660_@runat_05052006_121849_15963 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        Published_Applications_NA_New:*
```

```
 1:  /SIDS5/ptodata/1/pubpna/US08_NEW_PUB.seq1:*
 2:  /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 3:  /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 4:  /SIDS5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 5:  /SIDS5/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 6:  /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 7:  /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
 8:  /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
 9:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
10:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
11:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
12:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
13:  /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
14:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
15:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
16:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
17:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
18:  /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
19:  /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	155	100.0	111	18	US-11-145-463-6	Sequence 6, Appli
2	155	100.0	277	17	US-11-136-527-1878	Sequence 1878, Ap
3	155	100.0	277	17	US-11-136-527-5974	Sequence 5974, Ap
4	155	100.0	543	18	US-11-145-463-2	Sequence 2, Appli
5	155	100.0	1062	17	US-11-091-883-147	Sequence 147, App
6	155	100.0	1118	17	US-11-128-061-888	Sequence 888, App
7	155	100.0	1118	17	US-11-128-061-4530	Sequence 4530, Ap
8	155	100.0	1118	17	US-11-128-049-888	Sequence 888, App
9	155	100.0	1118	17	US-11-128-049-4530	Sequence 4530, Ap
10	155	100.0	1128	18	US-11-145-463-57	Sequence 57, Appl
11	151	97.4	90	17	US-11-175-690-119	Sequence 119, App
12	151	97.4	90	17	US-11-175-690-121	Sequence 121, App
13	151	97.4	90	17	US-11-175-690-122	Sequence 122, App
14	151	97.4	90	17	US-11-175-690-123	Sequence 123, App
15	151	97.4	90	17	US-11-175-690-125	Sequence 125, App
16	151	97.4	90	17	US-11-175-690-126	Sequence 126, App
17	151	97.4	90	17	US-11-175-690-127	Sequence 127, App
18	151	97.4	90	17	US-11-175-690-128	Sequence 128, App
19	151	97.4	90	17	US-11-175-690-129	Sequence 129, App
20	151	97.4	90	17	US-11-175-690-131	Sequence 131, App
21	151	97.4	90	17	US-11-175-690-132	Sequence 132, App
22	151	97.4	90	17	US-11-175-690-133	Sequence 133, App
23	151	97.4	90	17	US-11-175-690-134	Sequence 134, App
24	151	97.4	90	17	US-11-175-690-136	Sequence 136, App
25	151	97.4	90	17	US-11-175-690-137	Sequence 137, App
26	151	97.4	90	17	US-11-175-690-138	Sequence 138, App
27	91	58.7	600	17	US-11-136-527-5975	Sequence 5975, Ap
28	91	58.7	645	17	US-11-136-527-1879	Sequence 1879, Ap
29	90	58.1	111	17	US-11-175-690-188	Sequence 188, App
30	90	58.1	111	17	US-11-175-690-189	Sequence 189, App
31	90	58.1	111	18	US-11-145-463-40	Sequence 40, Appl
32	90	58.1	174	18	US-11-145-463-48	Sequence 48, Appl

SCORE Search Results Details for Application 10679746 and Search Result us-10-679-746-1.p2n.rst.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 10679746 and Search Result us-10-679-746-1.p2n.rst.

start

Go Back to previous page

```
                    GenCore version 5.1.8
            Copyright (c) 1993 - 2006 Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:         May  7, 2006, 02:13:39 ; Search time 2606 Seconds
                                        (without alignments)
                                        807.912 Million cell updates/sec

Title:          US-10-679-746-1
Perfect score:  155
Sequence:       1 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 30

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:      82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679746/runat_05052006_121840_15767/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10679746_@CGN_1_1_5315_@runat_05052006_121840_15767 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
                1:  gb_est1:*
```

```
 2:    gb_est2:*
 3:    gb_est3:*
 4:    gb_htc:*
 5:    gb_est4:*
 6:    gb_est5:*
 7:    gb_est6:*
 8:    gb_est7:*
 9:    gb_gss1:*
10:    gb_gss2:*
11:    gb_gss3:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	155	100.0	226	7	CK822603	CK822603 ig93d01.y
c	2	155	100.0	235	6	CA772135	CA772135 io96c04.x
c	3	155	100.0	235	6	CA774807	CA774807 ip12f09.x
	4	155	100.0	359	3	BI715164	BI715164 ic29g03.y
	5	155	100.0	369	3	BI349313	BI349313 ic69c07.y
	6	155	100.0	382	3	BM313323	BM313323 ig82f07.y
	7	155	100.0	384	6	CB178364	CB178364 is37e04.y
	8	155	100.0	389	5	BQ632756	BQ632756 il27e09.y
	9	155	100.0	394	2	BG654963	BG654963 ib44a12.y
	10	155	100.0	400	6	CB068992	CB068992 is33f09.y
	11	155	100.0	401	6	CA949891	CA949891 iq26h06.y
c	12	155	100.0	403	6	CA946915	CA946915 is12f03.x
	13	155	100.0	419	3	BM836042	BM836042 K-EST0111
	14	155	100.0	421	7	CK822370	CK822370 ig86a01.x
	15	155	100.0	425	8	DN351146	DN351146 LIB3579-0
	16	155	100.0	427	3	BI466966	BI466966 ic17d08.y
	17	155	100.0	428	3	BQ271407	BQ271407 ik13e06.y
	18	155	100.0	433	5	BU790431	BU790431 in51b02.y
	19	155	100.0	435	6	CA948735	CA948735 iq27a09.y
	20	155	100.0	437	5	BU074950	BU074950 im78h05.y
	21	155	100.0	441	6	CA842357	CA842357 ir26a06.y
	22	155	100.0	442	5	BU786403	BU786403 in54e01.y
	23	155	100.0	443	3	BQ271272	BQ271272 ik11g04.y
	24	155	100.0	450	6	CA843073	CA843073 ir53a03.y
	25	155	100.0	450	6	CA948774	CA948774 iq27f01.y
	26	155	100.0	451	3	BM503895	BM503895 ig97b05.y
c	27	155	100.0	451	5	BQ776591	BQ776591 il34g04.x
	28	155	100.0	451	6	CA952167	CA952167 iq15g12.y
	29	155	100.0	452	6	CB067109	CB067109 iq32b10.y
	30	155	100.0	453	6	CA943008	CA943008 ir67a10.y
	31	155	100.0	455	3	BM054456	BM054456 id57c08.y
	32	155	100.0	458	2	BG656237	BG656237 ib38g04.y
	33	155	100.0	459	3	BQ286311	BQ286311 ik28e04.y
	34	155	100.0	459	5	BU073715	BU073715 in23f12.y
	35	155	100.0	459	6	CA771516	CA771516 io72c08.y
	36	155	100.0	459	6	CA843551	CA843551 ir48f10.y
	37	155	100.0	459	6	CA866280	CA866280 ir36f08.y
	38	155	100.0	459	6	CA940994	CA940994 ir37a06.y
	39	155	100.0	460	5	BQ417426	BQ417426 ik37g09.y
	40	155	100.0	460	6	CA842633	CA842633 iq45b07.y
	41	155	100.0	461	3	BM312520	BM312520 ig75e12.y